

SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: Beach, David H.  
Demetrick, Douglas J.  
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Hannon, Gregory J.

(ii) TITLE OF INVENTION: Antibodies to Cell-Cycle Regulatory Proteins, and  
Uses Related Thereto

(iii) NUMBER OF SEQUENCES: 34

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WordPad

(vi) CURRENT APPLICATION DATA:

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(B) FILING DATE: 30-JAN-1998

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 15-JUL-1994

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 14-SEP-1994

(vii) PRIOR APPLICATION DATA:

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/227,371  
(B) FILING DATE: 14-APR-1994

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 18-NOV-1993

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 17-DEC-1992

(viii) ATTORNEY/AGENT INFORMATION:

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- (C) REFERENCE/DOCKET NUMBER: MIV-071.10

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 41..508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATG GAT CCG GCG GCG	55
Met Asp Pro Ala Ala	
1 5	
GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCC	103
Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala	
10 15 20	
CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG	151
Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu	
25 30 35	
CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG	199
Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met	
40 45 50	
ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG	247
Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu	
55 60 65	
CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT	295
Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala	
70 75 80 85	
GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG	343
Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly	
90 95 100	
GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG	391
Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu	
105 110 115	
GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT	439
Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala	
120 125 130	
GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA	487
Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu	
135 140 145	
GGT CCC TCA GAC ATC CCC GAT TGAAAGAACC AGAGAGGCTC TGAGAAACCT	538
Gly Pro Ser Asp Ile Pro Asp	

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 156 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:



(A) LENGTH: 837 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) NAME/KEY: CDS  
(B) LOCATION: 328..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGGACTCCG CGACGGTCCG CACCCTGCGG CCAGAGCGGC TTTGAGCTCG GCTGCTTCCG 60  
 CGCTAGGCGC TTTTTCCTCAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGCGCCAGGA 120  
 AAAGCCCAGG GCTAACGACC GGCCGCTCGG CACTGCACGG GGCCCCAAGC CGCAGAAGAA 180  
 GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTSCGCCGG 240  
 AGCAGCGTGG GAAAGAAGGG AAGAGTGTCG TTAAGTTTAC GGCCAACGGT GATTATCCG 300  
 GGCCGCTGCG CGTCTGGGGG CTGCGGA ATG CGC GAG GAG AAC AAG GGC ATG 351

Met Arg Glu Glu Asn Lys Gly Met

CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA 399  
 Pro Ser Gly Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly

CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC 447  
 Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn

GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC 495  
 Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly

AGC GCC CGC GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG CCC AAC 543  
 Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn

TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG 591  
 Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg

GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG GCG CGG 639  
 Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg

CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG 687  
 Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu

GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG 735  
 Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly

GAC TGACGCCAGG TTCCCCAGCC GCCCACAACG ACTTTATTTT CTTACCCAAT 788  
 Asp

TTCCACCCCC CACCCACCTA ATTCGATGAA GGCTGCCAAC GGGGAGCGG 837

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu  
 1 5 10 15  
 Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser  
 20 25 30  
 Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg  
 35 40 45  
 Ala Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu  
 50 55 60  
 Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr

65 70 75 80  
 Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val  
 85 90 95  
 Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly  
 100 105 110  
 Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala  
 115 120 125  
 Gly Tyr Leu Arg Thr Ala Thr Gly Asp  
 130 135

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 853 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 213..587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTTGGTC ACTGTAAGGA TTCAGCGCGC 60  
 GGGCCGCCCA CTCCAAGAGA GGGTTTCTCT GGTGAAGTTC GTGCGATCCC GGAGACCCAG 120  
 GACAGCGAGC TCGCTCTGG CTTTCGTGAA CATGTTGTTG AGGCTAGAGA GGATCTTGAG 180  
 AAGAGGGCCG CACCGGAATC CTGGACCAGG TG ATG ATG ATG GGC AAC GTT CAC 233  
 Met Met Met Gly Asn Val His  
 1 5  
 GTA GCA GCT CTT CTG CTC AAC TAC GGT GCA GAT TCG AAC TGC GAG GAC 281  
 Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp  
 10 15 20  
 CCC ACT ACC TTC TCC CGC CCG GTG CAC GAC GCA GCG CGG GAA GGC TTC 329  
 Pro Thr Thr Phe Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe  
 25 30 35  
 CTG GAC ACG CTG GTG GTG CTG CAC GGG TCA GGG GCT CGG CTG GAT GTG 377  
 Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg Leu Asp Val  
 40 45 50 55  
 CGC GAT GCC TGG GGT CGC CTG CCG CTC GAC TTG GCC CAA GAG CGG GGA 425  
 Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly  
 60 65 70  
 CAT CAA GAC ATC GTG CGA TAT TTG CGT TCC GCT GGG TGC TCT TTG TGT 473  
 His Gln Asp Ile Val Arg Tyr Leu Arg Ser Ala Gly Cys Ser Leu Cys  
 75 80 85  
 TCC GCT GGG TGG TCT TTG TGT ACC GCT GGG AAC GTC GCC CAG ACC GAC 521

Ser Ala Gly Trp Ser Leu Cys Thr Ala Gly Asn Val Ala Gln Thr Asp  
 90 95 100

GGG CAT AGC TTC AGC TCA AGC ACG CCC AGG GCC CTG GAA CTT CGC GGC 569  
 Gly His Ser Phe Ser Ser Ser Thr Pro Arg Ala Leu Glu Leu Arg Gly  
 105 110 115

CAA TCC CAA GAG CAG AGC TAAATCCGCC TCAGCCCGCC TTTTCTTCT 617  
 Gln Ser Gln Glu Gln Ser  
 120 125

TAGCTTCACT TCTAGCGATG CTAGCGTGTC TAGCATGTGG CTTTAAAAAA TACATAATAA 677

TGCTTTTTTTT GCAATCACGG GAGGGAGCAG AGGGAGGGAG CAGAAGGAGG GAGGGAGGGA 737

GGGAGGGACC TGGACAGGAA AGGAATGGCA TGAGAAACTG AGCGAAGGCG GCCGCGAAGG 797

GAATAATGGC TGGATTGTTT AAAAAATAA AATAAAGATA CTTTITAAAA TGTCAA 853

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly  
 1 5 10 15

Ala Asp Ser Asn Cys Glu Asp Pro Thr Thr Phe Ser Arg Pro Val His  
 20 25 30

Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly  
 35 40 45

Ser Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu  
 50 55 60

Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg  
 65 70 75 80

Ser Ala Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys Thr Ala  
 85 90 95

Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser Thr Pro  
 100 105 110

Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser  
 115 120 125

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 231 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCA CTC CTG GAA GCC GGC GCA GAT CCC AAC GCC CTG AAC CGC TTC GGG 48  
 Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly  
 1 5 10 15  
 AGG CGC CCA ATC CAG GTC ATG ATG ATG GGC AGC GCC AGG GTG GCA GAG 96  
 Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu  
 20 25 30  
 CTG CTG CTG CTC CAC GGA GCA GAA CCC AAC TGC GCC GAC CCT GCC ACC 144  
 Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr  
 35 40 45  
 CTT ACC AGA CCT GTG CAC GAC GCA GCT CGG GAA GGC TTC CTG GAC ACG 192  
 Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr  
 50 55 60  
 CTT GTC GTG CTG CAC CGG GCA GGG GCG CGG TTG GAT GTG 231  
 Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val  
 65 70 75

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly  
 1 5 10 15  
 Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu  
 20 25 30  
 Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr  
 35 40 45  
 Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr  
 50 55 60  
 Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val  
 65 70 75

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala  
 1 5 10 15  
 Tyr Gly Thr Val Tyr Lys Ala Xaa Asp Pro His Ser Gly His Phe Val  
 20 25 30  
 Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly  
 35 40 45  
 Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu  
 50 55 60  
 Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr  
 65 70 75 80  
 Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val  
 85 90 95  
 Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu  
 100 105 110  
 Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu  
 115 120 125  
 Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu  
 130 135 140  
 Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly  
 145 150 155 160  
 Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val  
 165 170 175  
 Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala  
 180 185 190  
 Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe  
 195 200 205  
 Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly  
 210 215 220  
 Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg  
 225 230 235 240



Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro  
 245 250 255  
 Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu  
 260 265 270  
 Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg  
 275 280 285  
 Ala Leu Gln His Ser Tyr Leu His Lys Asp Glu Gly Asn Pro Glu  
 290 295 300

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 326 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Glu Lys Asp Gly Leu Cys Arg Ala Asp Gln Gln Tyr Glu Cys Val  
 1 5 10 15  
 Ala Glu Ile Gly Glu Gly Ala Tyr Gly Lys Val Phe Lys Ala Xaa Asp  
 20 25 30  
 Leu Lys Asn Gly Gly Arg Phe Val Ala Leu Lys Arg Val Arg Val Gln  
 35 40 45  
 Thr Gly Glu Glu Gly Met Pro Leu Ser Thr Ile Arg Glu Val Ala Val  
 50 55 60  
 Leu Arg His Leu Glu Thr Phe Glu His Pro Asn Val Val Arg Leu Phe  
 65 70 75 80  
 Asp Val Cys Thr Val Ser Arg Thr Asp Arg Glu Thr Lys Leu Thr Leu  
 85 90 95  
 Val Phe Glu His Val Asp Gln Asp Leu Thr Thr Tyr Leu Asp Lys Val  
 100 105 110  
 Pro Glu Pro Gly Val Pro Thr Glu Thr Ile Lys Asp Met Met Phe Gln  
 115 120 125  
 Leu Leu Arg Gly Leu Asp Phe Leu His Ser His Arg Val Val His Arg  
 130 135 140  
 Asp Leu Lys Pro Gln Asn Ile Leu Val Thr Ser Ser Gly Gln Ile Lys  
 145 150 155 160

Leu Ala Asp Phe Gly Leu Ala Arg Ile Tyr Ser Phe Gln Met Ala Leu  
165 170 175

Thr Ser Val Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu  
180 185 190

Gln Ser Ser Tyr Ala Thr Pro Val Asp Leu Trp Ser Val Gly Cys Ile  
195 200 205

Phe Ala Glu Met Phe Arg Arg Lys Pro Leu Phe Arg Gly Ser Ser Asp  
210 215 220

Val Asp Gln Leu Gly Lys Ile Leu Asp Val Ile Gly Leu Pro Gly Glu  
225 230 235 240

Glu Asp Trp Pro Arg Asp Val Ala Leu Pro Arg Gln Ala Phe His Ser  
245 250 255

Lys Ser Ala Gln Pro Ile Glu Lys Phe Val Thr Asp Ile Asp Glu Leu  
260 265 270

Gly Lys Asp Leu Leu Leu Lys Cys Leu Thr Phe Asn Pro Ala Lys Arg  
275 280 285

Ile Ser Ala Tyr Ser Ala Leu Ser His Pro Tyr Phe Gln Asp Leu Glu  
290 295 300

Arg Cys Lys Glu Asn Leu Asp Ser His Leu Pro Pro Ser Gln Asn Thr  
305 310 315 320

Ser Glu Leu Asn Thr Ala  
325

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly  
1 5 10 15

Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val  
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His  
 35 40 45  
 Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro  
 50 55 60  
 Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu  
 65 70 75 80  
 Arg Xaa Ala Xaa Gly  
 85

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu  
 1 5 10 15  
 Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu  
 20 25 30  
 Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro  
 35 40 45  
 Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu  
 50 55 60  
 Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa  
 65 70 75 80  
 Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val  
 85 90 95  
 Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly  
 100 105 110  
 Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa  
 115 120 125  
 Xaa Tyr Leu Arg Xaa Ala Xaa Gly Gly Thr Arg Gly Ser Asn His Ala  
 130 135 140  
 Arg Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp

145

150

155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu  
1 5 10 15

Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser  
20 25 30

Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg  
35 40 45

Ala Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu  
50 55 60

Leu Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa  
65 70 75 80

Xaa Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu  
85 90 95

Val Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp  
100 105 110

Gly Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa  
115 120 125

Xaa Xaa Tyr Leu Arg Xaa Ala Xaa Gly Asp  
130 135

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly  
1 5 10 15  
Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val  
20 25 30  
His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His  
35 40 45  
Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro  
50 55 60  
Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu  
65 70 75 80  
Arg Xaa Ala Xaa Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys  
85 90 95  
Thr Ala Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser  
100 105 110  
Thr Pro Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Ala Glu Ile Gly Xaa Gly Ala Tyr Gly Xaa Val Xaa Lys Ala Arg Asp  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Xaa Lys Ala Arg Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ala Arg Asp  
1

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 960 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAGAGGGA ATTCGACACGA GGCAGCATG GAGCCTTCGG CTGACTGGCT GGCCACGGCC	60
GCGGCCCCGGG GTCCGGTAGA GGAGGTGCGG GCGCTGCTGG AGGCGGTGGC GCTGCCCCAA	120
CGCACCGAAT AGTTACGGTC GGAGGCCGAT CCAGGTCATG GATGATGGGC AGCGCCCCGA	180
GTGGCGGAGC TCTGCTGCT CCACGGCGCG GAGCCCAACT GCGCCGACCC CGCCACTCTC	240
ACCCGACCCG TGCACCACGC TGCCCGGGAG GGCTTCTGGA CACGCTGGTG GTGCTGCACC	300
GGGCCGGGGC GCGGCTGGAC GTGCGCGATG CCTGGGGCCG TCTGCCCGTG GACCTGGCTG	360
AGGAGCTGGG CCATCGCGAT GTCGCACGGT ACCTGCGCGC CCGTGCGGGG GGCACCAGAG	420

GCAGTAACCA TGCCCGCATA GATGCCGCGG AAGGTCCCTC AGACATCCCC GATTGAAAGA 480  
ACCAGAGAGG CTCTGAGAAA CCTCGGGAAA CTTAGATCAT CAGTCACCGA AGGTCCTACA 540  
GGGCCACAAC TGCCCCCGCC ACAACCCACC CCGCTTTCGT AGTTTTTCATT TAGAAAATAG 600  
AGCTTTTAAA AATGTCCTGC CTTTAAACGT AGATATAAGC CTTCCCCCAC TACCGTAAAT 660  
GTCCATTTAT ATCATTTTTT ATATATTCTT ATAAAAATGT AAAAAAAGAA AAACACCGCT 720  
TCTGCCTTTT CACTGTGTTG GAGTTTCTG GAGTGAGCAC TCACGCCCTA AGCGCACATT 780  
CATGTGGGCA TTTCTTGCGA GCCTCGCAGC CTCCGGAAGC TGTGCACTTC ATGACAAGCA 840  
TTTGTGAAC TAGGGAAGCT CAGGGGGGTT ACTGGCTTCT CTTGAGTCAC ACTGCTAGCA 900  
AATGGCAGAA CCAAAGCTCA AATAAAAATA AAATTATTTT CATTCAATCA CTCAAAAAAA 960

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 334 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGNGGNAAGN TGTGGGGGAA AGTTTGGGGA TGGAANACCA ANCCCTCCTT TCNTTACCAA 60  
ACNCTGGCTC TGNCGAGGCT NCNTCCGANT GGTNCCCCCG GGGGAGACCC AACCTGGGNC 120  
GACTTCAGGG NTGCNACATT CATTCATAA GTGCTNGGAG NTAATANCAC CTCCTCCGAG 180  
CANNGACAGG NTCGAGGGG GCTCTTCCCC CANCACCGGA GGAAGAAAGA GGAGGGNCTN 240  
CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATGGATCCGG CGGCGGGGAG 300  
CAGCATGGAN CCTTCGACTG ACTGACTGCC TCGC 334

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 368 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCNCTTATTG NTAGGANATA ATAACACCTC CACCGATAAC TTCACCTACA ACGTCCCNTT 60  
TCCTGGAAAG ATACACAGCG TTCCCTCCAG AGGATTGTGT GGACAGGGTN GGAGNGGTCT 120  
CTTCCNCCAC CACCGGAGGA AGAAAGAGGA GGGGCTGNCT GTTCACGAGA GGGTGGGACG 180  
GACCNCGTAC GCTCGNCGNC TNCGGAGAGG GGGAGAGCAT CANCGGNCGN CGGGGAGCAA 240  
CATGGAACCG NCGGCGGGGA GCAGCATGGA NCCTTCGGCT GACTGGCTGN CCACGNCCAC 300  
GNCCCGGGGT CGGGTAGAGG AGGTGCGGNC GCTNCTGGAG GCGGGGNCTC TGNCCAACNC 360  
GCTAAAN 368

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 404 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACNNCTCC GGCCGGNGTC GGGTAGAGGA GGTGCGGGCG CTGCTGGAGG CGGGGGCGCT 60  
GCCCAACGCA CCGAATAGTT ACGGTCGGAG GCCGATCCAG GTNNGGGTAG AGGGTCTGCA 120  
GCGGGAGCAG GGGATGGCGG GCGACTCTGG AGGACGAAGT TTGCAGGGGA ATTGGAATCA 180  
GGTAGCGCTT CGATTCTCCN GAAAAAGGGG AGGCTTCCTG GGGAGTTTTT AGAAGGGGTT 240  
TGTAATCACA GACCTCCTCC TGGCGACGTC CTGGGGGCTT GGAAGCCAA GGAAGAGGAA 300  
TNAGGAGCCA CGCGGTACG AGTCTCTCGA ATGCTGAGAA GATCTNAAGG GGGGAACATA 360  
TTTGTATTAG CNTCCAAGTN TNCTCTNTAT CANATACAAA NTNC 404

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 401 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCTNANCCC GGGTAGAGGG TCTGCAGCGG GAGCAGNGGA TGGCGGGCGA CTCTGGAGGA 60  
 CGAAGTTGGC AGGGGAATTG GAATCAGGTA GCGCTTCGAN TCTCCGAAA AAGGGGAGGC 120  
 TTCCTGGGGA GTTNNCAGAA GGGGTTTGTA ATCACAGNCC TCCNCCTGGC GACGCCCTGG 180  
 GGGGTTGGGA AGCCAAGGAA GAGGAATGAG GAGNCACGCG CNTACAGNTC TCTCGAATNC 240  
 TGANAAGATC TGAAGGGGGG AACATATTTG TATTAGNATN NAAGTATGCT CTTTATCAGA 300  
 TAGAAAATTC ACGAACGTGT GGNATAAAAA GGGAGTCTTA AAGAAATNTA AGATGTGCTG 360  
 GGACTACTTA GCCTCCAANA CACAGATNCC TGGATGGAGC T 401

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAAANNAAAA AAAATCTCCC AGGCCTAACA TAATTNTCAG GAAAGAAATT TCAGTAGTTG 60  
 NATCTCAGGG GAAATACAGG AAGTTAGCCT GGAGTAAAAG TCAGTGTGTC CCTGCCCCCTT 120  
 TGCTANATTG CCCGTGCCTC ACAGTGCTCT CTGCCTGTGA CGACAGCTCC NCAGAAAGTTC 180  
 GGAGGATATA ATGGAATTCA TTGTGTACTG AAGAATGGAT AGAGAACTCA AGAAGGAAAT 240  
 TGGAAACTGG AAGCAAATGT AGGGGTAATT AGACACCTGG GGCTTCTGTG GGGGTCTGCT 300  
 TGGCGGTGAG GGGGCTCTAC ACAAGCTTCC TTTCCGTCAT GCCGNCCCCC ACCCTGGCTC 360  
 TGACCATTCT GTTCTCTCTG GCAGGTCATG ATGATGGGCA GCGCCCGAGG CGCGGAGCTG 420  
 CTGCTGCTCC ACGGCGCGGA GCCCACTGCT CCGACGCCG 459

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

① 1  
AANAAAAAG AAATNGATAA NATAGAGGAA TGAACANATT AAAATCAAAA AACANAACAN 60  
AGACATAATA AAAAACGAGA ATGTTCTAGA CNTAATCATA ATTATAAAGC TCAAGACTCA 120  
TTGATATNAA GGADATTGAA GGGAAATCTT AACTAGCACA ANNGNATNAA AAAANAATTC 180  
CCACGACACC GCCACTCTCA ACGCATCCGT GCTCGACACT GCCCGGGAGG TCNTCCTGGA 240  
CACGCTGGTG GTNCTCCACC GGNCCGGGGC ACGTCTGGAC GTGCGCGATG CCTGGGNCCG 300  
NCTACCCGTG GTACCTGACT GAGGACCTGG GCCATCCCGA TTTCGCNGGG TANCTCNGN 360  
GGCTGNGGGG GCCAANAGAG GNCANTACCC 390

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 214 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCTGCNACGA CCCCGCCACT CTCACCCGAC CCGTGACGA CGCTGTCCGG GAGGGTTTCC 60  
TGGACACGCT GGTGGTGCTG CACCGGGCCG GGGNGCGTT GGACGTGCGC GATGCCTGGG 120  
GCCGCCTNCC CGTGGNACCT GGTGAGGAG CTGGGNCATC GCGATGTCGC ACGGTACCTG 180  
CGCGCGTTGC GGGGGGCACC AGAGGNNAGT NACC 214

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

NCTCTCACGG TGGGGAGGCC AACTGCGCCG AACCCGCCAC TCTCACCCGA CCCGCGCACG	60
ACGGTGCCCCG GGAGGGGTTC CTGGACACGC TGGTGGTGCT GCACCGGGCC GGGGCGCGGC	120
TGGACGTTTCG NGATGCCTGG GGGNTCTNTC CGTNGNACCT GGCTGAAGAG CTGCNNCATC	180
GNGATGTCGC ACGGCCNCTG TGTGNGGNTG CGGGGGGCAC CATAGGTCAG TNTCC	235

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NAAGTATGAG CGAAACNAAT TGTGGTTTGA GAANAGGNAA TCGTAGGGAA CTTCGGGATC	60
CCNCNGGGAN CNCCAGAACC TGAGNCGCCN ATTGGAAATN ACAAACTGNC TGNATCACTC	120
CGNACCAGGT NCAAAAGATA CCTGGGGANG CGGGAAGGGA AAGACNACAT CNAGACCGCC	180
TTCGCNCCTN GGNATTGTGA GCAGCCTCTG AGACTCATTN ATATNACACT CTCGTNTTTC	240
TTCTTACAAC CCTGCGGNCC GCGCGGTCGC GCTTCTCTG CCCTCCGCCG GGTGGACCTG	300
GAGCGCTTGA GCGGTCGGCG CGCCTGGAGC AGCCAGGCGG NCAGTGGACT AGCTGCTGGA	360
CCAGGGAGGT GTGGGAGAGC GGTGGCGGCG GGTACATGCA CGTGAAGCCA TTGCGAGAAC	420
TTTATCCATA AGTATTTCAA TACCGGTAGG GACGGCAAGA GAGGAGGGCG GGATGTGCCA	480
CACATCTTTG ACCTCAGGT TCTAACGCCT GTTTCTTTC TGCCCTCTGC AGACAACCCC	540
CGATTGAAAG AACCAGAGAG GCTCTGAGAA ACC	573

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCCATCGCG CCTTGGGANT GTGAGCNACC ATTGAGACTC ATNAATATAG CACTCGTTTT	60
TCTTCTTGCA ACCCTGCCCN CCGCGCGGTC GCGCTNTCTC TGCCCTCCGC NGGGTGGACC	120
TGGAGCGAGC GCTTGAGCGG TCGGTCGGCG CNCCTGGANC AGCCAGGCGG GCAGTGGACT	180
ACCTNCTGGA CCAGGGACCT GTGGGAGAGC GGTGNCGGCG GGTACATGCA CGTGAAGCCA	240
TTGCGAGAAC TTTATCCATA AGTATTTCAA TGCCGGTAGG GACGGCAAGA GAGGAGGGCG	300
GGATGTNCCA CACATCTTTG ACCTCAGGTT TCTAACGCCT GTTTTCTTTC TGCCCTCTGC	360
AGACATCCCC GATTGAAAGA ACCAGAGAGG CTCTGAGAAA CCTCCGAAA CTTAGNTCAT	420
CANTCGCCGN AAAA	434

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGAAATTAGA TCATCAGTCA CCGATCCTCC TACAGGGNCA CAACTGNCCC CGCCACAACC	60
CACCCCGNTT TCGTAGTTTT CATTTAGAAA ATAGAGCTTT TAAAAATGTC CTGCCTTTTA	120
ACGTAGATAT ATGCCTTCCC CCACTACCGN AAATGTCCAT TTATATCATN TTTTATATAT	180
TCTTATAAAA ATGTAAAAA GAAAAACACC GCTTCTGCCT TTTCAGTGTG TTGGAGTTTT	240
CTGGAGTGAG CACTCACGCC CTAAGCGCAC ATTCATGTGG GCATTTCTTG CGAGCCTCGC	300
AGNCTCCGGA AGCTGTGAC CTCGAGGGGG GGNCCGGTAC CCAATTCGCC CTATAGTGAG	360
TCGTATTACA ATTCAGTGGN CGNCGNTTTT ACAACGTCGG TGGACTGGGA AAACCCCGGN	420
GTTACCCAAC TTTAATCGNC TTGGAGGACA TCCCCCTTTT CGCCAGNTGG GGTATAGNG	480
AAGAGGGCCN CACCNNTCGC CC	502

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

91

CANCNATNTN	CGGCATTTCT	NGNGAGCCTC	GTAGTCTCCG	GATGNTGTCG	ACCTCGAGGG	60
GGGGNCCNGT	ACCCAATTCG	NCCTATNGTG	AGTCGTNTTA	CAATTCCTG	GCCGCCGTTT	120
TNACAACGTC	GNTGNACTGG	GAAAACCCTG	GTGTTACCCA	ACTTNAATGT	CCTTGNAGNA	180
CATCCCCCTT	TNCGCCAGCT	GGTGTAATAG	CGANGAGGCC	CGCACCGATC	GCCCTTCCCA	240
ACAGTTGNGC	AGCCTGAATG	GCGAATGGAA	ATTGTAAGCG	TTAATATTTT	GTAAAAATTC	300
GCGTTANATC	NTCGGTTAAN	TCAGCTCATN	TTTTATCCAA	TAGGCCGANA	TCGGCANAAT	360
CCCCAATAAA	TCAANAGAAT	AGACCGAGAT	AGGGTTGAGT	GTCGTTCCAG	TTNGGGAACA	420
NGAGTCCACT	ATTAAAGANC	GTAGNCTCNA	ACGTCANAGG	GCGAAAAACC	NTNTTTCAGN	480
GGATTGGNCC	ACTACGCNTA	NCC				503

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 515 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CANCNATNTN	CGGCATTTCT	NGNGAGCCTC	GTAGTCTCCG	GATGNTGTCG	ACCTCGAGGG	60
GGGGNCCNGT	ACCCAATTCG	NCCTATNGTG	AGTCGTNTTA	CAATTCCTG	GCCGCCGTTT	120
TNACAACGTC	GNTGNACTGG	GAAAACCCTG	GTGTTACCCA	ACTTNAATCG	CCTTGNAGNA	180
CATCCCCCTT	TNCGCCAGCT	GGTGTAATAG	CGANGAGGCC	CGCACCGATC	GCCCTTCCCA	240
ACAGTTGNGC	AGCCTGAATG	GCGAATGGAA	ATTGTAAGCG	TTAATATTTT	GTAAAAATTC	300
GCGTTANATC	NTCGGTTAAN	TCAGCTCATN	TTTTATCCAA	TAGGCCGANA	TCGGCANAAT	360
CCCCAATAAA	TCAANAGAAT	AGACCGAGAT	AGGGTTGAGT	GTCGTTCCAG	TTNGGGAACA	420

NGAGTCCACT ATTAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAAACC NTNTTTCAGN 480  
GGATTGGNCC ACTACGCNTA NCCATCACCC TATTC 515

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 89 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu  
1 5 10 15  
His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val  
20 25 30  
His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg  
35 40 45 50  
Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp  
55 60 65  
Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala  
70 75 80 85  
Ala Gly Gly Thr

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu

1	5	10	15
His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val			
20	25	30	
His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg			
35	40	45	50
Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp			
55	60	65	
Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala			
70	75	80	85
Ala Gly Asp			

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